

BLASTN 2.2.19+

Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: URUK3T33016

Database: Nucleotide sequences derived from the Patent division of GenBank

8,753,385 sequences; 4,832,233,817 total letters

Query= SID_3

Length=2660

Sequences producing significant alignments:		Score (Bits)	E Value
dbj DI129697.1	AN EXPRESSION CASSETTE AND VECTOR FORTRANSIEN...	4817	0.0
dbj DI109112.1	FLP-mediated Recombination	4817	0.0
dbj DJ052243.1	FLP-mediated Recombination	4817	0.0
dbj DD418156.1	AN EXPRESSION CASSETTE AND VECTOR FOR TRANSIE...	4817	0.0
dbj E00140.1	Genomic DNA encoding human growth hormone	4795	0.0
emb AX719120.1	Sequence 1 from Patent EP1295938	4724	0.0
emb AX659146.1	Sequence 1 from Patent WO02101002	4724	0.0
emb CS741886.1	Sequence 9882 from Patent WO2005083127	4684	0.0
emb CS741885.1	Sequence 9881 from Patent WO2005083127	4684	0.0
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gb GC699294.1	Sequence 14539 from patent US 6812339	2802	0.0
gb GC699293.1	Sequence 14538 from patent US 6812339	2802	0.0
gb GC699292.1	Sequence 14537 from patent US 6812339	2802	0.0
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dbj DI151081.1	Methods And Constructs For Expressing Polypep...	1068	0.0
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>dbj|DI109112.1| FLP-mediated Recombination
Length=2660

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Score = 4817 bits (2608), Expect = 0.0
Identities = 2660/2660 (100%), Gaps = 0/2660 (0%)
Strand=Plus/Plus

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>dbj|DJ052243.1| FLP-mediated Recombination
Length=2660

Score = 4817 bits (2608), Expect = 0.0
Identities = 2660/2660 (100%), Gaps = 0/2660 (0%)
Strand=Plus/Plus

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>dbj|DD418156.1| AN EXPRESSION CASSETTE AND VECTOR FOR TRANSIENT OR STABLE EXPRESSION OF EXOGENOUS MOLECULES
Length=2660

Score = 4817 bits (2608), Expect = 0.0
Identities = 2660/2660 (100%), Gaps = 0/2660 (0%)
Strand=Plus/Plus

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Query   2341  CGATTCCAGGCATGCAAGACCAGGCTCAGCTAAATTTTGTATTTTGGTAGAGACGGGGT  2400
          |||
Sbjct  2341  CGATTCCAGGCATGCAAGACCAGGCTCAGCTAAATTTTGTATTTTGGTAGAGACGGGGT  2400
Query   2401  TTCACCATATTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCGCCCGCCTCGG  2460
          |||
Sbjct  2401  TTCACCATATTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCGCCCGCCTCGG  2460
Query   2461  CCTCCCAAAATGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCCCTGTCTGTGATTT  2520
          |||
Sbjct  2461  CCTCCCAAAATGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCCCTGTCTGTGATTT  2520
Query   2521  TAAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGCTACCTGGCCATGCC  2580
          |||
Sbjct  2521  TAAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGCTACCTGGCCATGCC  2580
Query   2581  AGCCAGTTGGACATTGAGTTGTTTGCTTGGCACTGTCTCTCATGCAATTGGGTCACCT  2640
          |||
Sbjct  2581  AGCCAGTTGGACATTGAGTTGTTTGCTTGGCACTGTCTCTCATGCAATTGGGTCACCT  2640
Query   2641  AGTAGATGCTTGTGTAATTC  2660
          |||
Sbjct  2641  AGTAGATGCTTGTGTAATTC  2660

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>dbj|E00140.1| Genomic DNA encoding human growth hormone
Length=2660

Score = 4795 bits (2596), Expect = 0.0
Identities = 2656/2660 (99%), Gaps = 0/2660 (0%)
Strand=Plus/Plus

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Query   1      GAATTCAGCACTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCT  60
          |||
Sbjct   1      GAATTCAGCACTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCT  60
Query   61      TTTCACACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG  120
          |||
Sbjct   61      TTTCACACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG  120
Query   121     GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGCTCTCAAGGACTGGCCTATCCTGACA  180
          |||
Sbjct   121     GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGCTCTCAAGGACTGGCCTATCCTGACA  180
Query   181     TCCTTCTCCGCGTTTCAGGTTGGCCACCATGGCCTGCTGCCAGAGGGACCCACGTGACCC  240
          |||
Sbjct   181     TCCTTCTCCGCGTTTCAGGTTGGCCACCATGGCCTGCTGCCAGAGGGACCCACGTGACCC  240
Query   241     TTAAAGAGAGGACAAGTTGGGTGGTATCTCTGGCTGACATTCTGTGCACAACCTCACAA  300
          |||

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Sbjct 241 TTAAGAGAGGACAAGTTGGGTGGTATCTCTGGCTGACATTCTGTGCACAACCCCTCACAA 300
Query 301 CGCTGGTGATGGTGGGAAGGAAAGATGACAAGTCAGGGGGCATGATCCAGCATGTGTG 360
      |||
Sbjct 301 CGCTGGTGATGGTGGGAAGGAAAGATGACAAGTCAGGGGGCATGATCCAGCATGTGTG 360
Query 361 GGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCTAAACATG 420
      |||
Sbjct 361 GGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCTAAACATG 420
Query 421 CAGAGAAACAGGTGAGGAGAAGCAGCGAGAGAGAAGGGGCCAGGTATAAAAAGGGCCAC 480
      |||
Sbjct 421 CAGAGAAACAGGTGAGGAGAAGCAGCGAGAGAGAAGGGGCCAGGTATAAAAAGGGCCAC 480
Query 481 AAGAGACCAGCTCAAGGATCCCAAGGCCCACTCCCCGAACCACTCAGGGTCTGTGGAC 540
      |||
Sbjct 481 AAGAGACCAGCTCAAGGATCCCAAGGCCCACTCCCCGAACCACTCAGGGTCTGTGGAC 540
Query 541 AGCTCACTAGCGGCAATGGTGCAGGTAAAGCGCCCTAAAAATCCCTTTGGCACAATGTGT 600
      |||
Sbjct 541 AGCTCACTAGCGGCAATGGTGCAGGTAAAGCGCCCTAAAAATCCCTTTGGCACAATGTGT 600
Query 601 CCTGAGGGGAGAGGCGGCGTCCCTGTAGATGGGACGGGGGCACTAACCTCAGGTTTGGGG 660
      |||
Sbjct 601 CCTGAGGGGAGAGGCGGCGTCCCTGTAGATGGGACGGGGGCACTAACCTCAGGTTTGGGG 660
Query 661 CTTATGAATGTTAGCTATCGCCATCTAAGCCCAAGTATTGGCCCAATCTCTGAATGTTCT 720
      |||
Sbjct 661 CTTATGAATGTTAGCTATCGCCATCTAAGCCCAAGTATTGGCCCAATCTCTGAATGTTCT 720
Query 721 GGTCCCTGGAGGAGGCagagagagagagagagagagagagagagagagagagagagagagag 780
      |||
Sbjct 721 GGTCCCTGGAGGAGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Query 781 GAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTGCTCCGGTTTCTCCCCAGGCTC 840
      |||
Sbjct 781 GAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTGCTCCGGTTTCTCCCCAGGCTC 840
Query 841 CCGGACGTCCTCGCTCTGGCTTTTGGGCTGCTCTGCCGTGCTCGGCTTCAAGAGGGCAG 900
      |||
Sbjct 841 CCGGACGTCCTCGCTCTGGCTTTTGGGCTGCTCTGCCGTGCTCGGCTTCAAGAGGGCAG 900
Query 901 TGCCTTCCCAACCAATTCCTTATCCAGGCTTTTGGACAACGCTATGCTCCGCGCCGTCG 960
      |||
Sbjct 901 TGCCTTCCCAACCAATTCCTTATCCAGGCTTTTGGACAACGCTATGCTCCGCGCCGTCG 960
Query 961 CCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAAAGCTCTTGGGTAAATGGGTGC 1020
      |||
Sbjct 961 CCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAAAGCTCTTGGGTAAATGGGTGC 1020
Query 1021 GCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCTGGGAAGTAATGGGAGGAGACTA 1080
      |||
Sbjct 1021 GCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCTGGGAAGTAATGGGAGGAGACTA 1080
Query 1081 AGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGATGAGCATACGCTGAGTGAG 1140
      |||
Sbjct 1081 AGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGATGAGCATACGCTGAGTGAG 1140
Query 1141 GTTCCAGAGAAAGTAACAATGGGAGCAGGTCTCCAGCATAGACCTTGGTGGGCGGTCTT 1200
      |||

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Sbjct  2041  TGGCATCCCTGTGACCCCTCCCCAGTGCCCTCTCCTGGTCGTGGAAGGTGCTACTCCAGTG  2100
Query  2101  CCCACCAGCCTTGTCTTAATAAAATTAAGTTGCATCATTTTGTGTTAGTAGGTGTCCTTG  2160
      |||
Sbjct  2101  CCCACCAGCCTTGTCTTAATAAAATTAAGTTGCATCATTTTGTGTTAGTAGGTGTCCTTG  2160
Query  2161  TATAATATTATGGGGTGGAGGCGGGTGGTATGGAGCAAGGGGCCAGGTTGGGAAGACAAC  2220
      |||
Sbjct  2161  TATAATATTATGGGGTGGAGGCGGGTGGTATGGAGCAAGGGGCCAGGTTGGGAAGACAAC  2220
Query  2221  CTGTAGGGCCTTCAGGGTCTATTTCGGAACACAGGCTGGAGTGCAGTGGCAGTCTTGGCTC  2280
      |||
Sbjct  2221  CTGTAGGGCCTTCAGGGTCTATTTCGGAACACAGGCTGGAGTGCAGTGGCAGTCTTGGCTC  2280
Query  2281  GCTGCAATCTCCGCCCTCTGGGTTCAAGCGATTCTCTGCCTCAGTCTCCCGAATAGTTG  2340
      |||
Sbjct  2281  GCTGCAATCTCCGCCCTCTGGGTTCAAGCGATTCTCTGCCTCAGTCTCCCGAATAGTTG  2340
Query  2341  CGATTCCAGGCATGCAAGACCAGGCTCAGCTAATTTTGTATTTTGGTAGAGACGGGGT  2400
      |||
Sbjct  2341  GGATTCCAGGCATGCAAGACCAGGCTCAGCTAATTTTGTATTTTGGTAGAGACGGGGT  2400
Query  2401  TTCACCATATTTGGCCAGTCTGGICTCCATCTCCTGACCICAGGTAATCCGCCCGCCTCGG  2460
      |||
Sbjct  2401  TTCACCATATTTGGCCAGTCTGGICTCCATCTCCTGACCICAGGTAATCCGCCCGCCTCGG  2460
Query  2461  CCTCCCAAAATGTCTGGGATTACAGGTATGAGCCACTGGGCCCTTCCCTGTCTGTGATTT  2520
      |||
Sbjct  2461  CCTCCCAAAATGTCTGGGATTACAGGTATGAGCCACTGGGCCCTTCCCTGTCTGTGATTT  2520
Query  2521  TAAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGCTACCTGGCCATGCC  2580
      |||
Sbjct  2521  TAAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGCTACCTGGCCATGCC  2580
Query  2581  AGCCAGTTGGACATTTGAGTTGTTTGCTTGGCACTGTCTCTCATGCATTGGGTCCACTC  2640
      |||
Sbjct  2581  AGCCAGTTGGACATTTGAGTTGTTTGCTTGGCACTGTCTCTCATGCATTGGGTCCACTC  2640
Query  2641  AGTAGATGCTTGTGTAATTC  2660
      |||
Sbjct  2641  AGTAGATGCTTGTGTAATTC  2660

>emb|AX719120.1| Sequence 1 from Patent EP1295938
Length=5002

Score = 4724 bits (2558), Expect = 0.0
Identities = 2651/2668 (99%), Gaps = 13/2668 (0%)
Strand=Plus/Plus

Query  1  GAATTCAGCAGCTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCT  60
Sbjct  1589  GAATTCAGCAGCTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCT  1648
Query  61  TTTCACACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATCGGGGAGGAGGAAAG  120
      |||
Sbjct  1649  TTTCACACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATCGGGGAGGAGGAAAG  1708
Query  121  GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGGCCTATCTCGACA  180
      |||

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Sbjct	2606	TGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCTGGGAAGTAATGGGAGGAGA	2665
Query	1078	CTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGATGAGCATACGCTGAGT	1137
Sbjct	2666	CTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGATGAGCATACGCTGAGT	2725
Query	1138	GAGGTTCCCGAAAAAGTAACAATGGGAGCAGGTCTCCAGCATAGACCTTGGTGGGCGGTC	1197
Sbjct	2726	GAGGTTCCCGAAAAAGTAACAATGGGAGCAGGTCTCCAGCATAGACCTTGGTGGGCGGTC	2785
Query	1198	CTTCTCCTAGGAAGAAGCCTATATCTCTGAAGGAGCAGAAGTATTCTCTCGCAAAACC	1257
Sbjct	2786	CTTCTCCTAGGAAGAAGCCTATATCTCTGAAGGAGCAGAAGTATTCTCTCGCAAAACC	2845
Query	1258	CCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAACGCA	1317
Sbjct	2846	CCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAACGCA	2905
Query	1318	GCAGAAATCTGTGAGTGGATGCCCTTCTCCCGAGGTGGGATGGGGTAGACCTGTGGTCAGA	1377
Sbjct	2906	GCAGAAATCTGTGAGTGGATGCCCTTCTCCCGAGGTGGGATGGGGTAGACCTGTGGTCAGA	2965
Query	1378	GCCCCGGGCGAGCAGCCACTGCCGGTCCCTTCCCTGCAGAACCTAGAGCTGCTCCGCA	1437
Sbjct	2966	GCCCCGGGCGAGCAGCCACTGCCGGTCCCTTCCCTGCAGAACCTAGAGCTGCTCCGCA	3025
Query	1438	TCTCCCTGCTGCTCATCCAGTCAATGGCTGGAGCCCGTGACGCTCCTCAGGAGCGTCTTCG	1497
Sbjct	3026	TCTCCCTGCTGCTCATCCAGTCAATGGCTGGAGCCCGTGACGCTCCTCAGGAGCGTCTTCG	3085
Query	1498	CCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGCTCTATCGCCACCTGAAGGACCTAG	1557
Sbjct	3086	CCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGCTCTATCGCCACCTGAAGGACCTAG	3145
Query	1558	AGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAGG-ATCC--AATCTGGGG	1614
Sbjct	3146	AGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAGGGATCCCAATCTCTGGGG	3205
Query	1615	CCCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTCTTTTATGAGTCAGG	1674
Sbjct	3206	CCCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTCTTTTATGAGTCAGG	3265
Query	1675	CGCTGACCCAAGAGAACTCACCCTATTCTTCAATTTCCCTCGTGAATCTCCAGGCCCTT	1734
Sbjct	3266	CGCTGACCCAAGAGAACTCACCCTATTCTTCAATTTCCCTCGTGAATCTCCAGGCCCTT	3325
Query	1735	CTCTACAACCTGGAGGGGAGGGAGGAAAAATGGATGAATGAGAGAGGGAGGGAAACAGTGCC	1794
Sbjct	3326	CTCTACAACCTGGAGGGGAGGGAGGAAAAATGGATGAATGAGAGAGGGAGGGAAACAGTGCC	3385
Query	1795	CAAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTTGAGAGGCTGGAAGATGGCAGCCCC	1854
Sbjct	3386	CAAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTTGAGAGGCTGGAAGATGGCAGCCCC	3445
Query	1855	CGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAAATCGCACAAACGAT	1914
Sbjct	3446	CGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAAATCGCACAAACGAT	3505
Query	1915	GACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGGTC	1974

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Sbjct 3506 GACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGGTC 3565
Query 1975 GAGACATTCTCGCGCATCGTGCAGTGC CGCCTCTGTGGAGGGCAGCTGTGGCTTCTAGCTG 2034
          |||
Sbjct 3566 GAGACATTCTCGCGCATCGTGCAGTGC CGCCTCTGTGGAGGGCAGCTGTGGCTTCTAGCTG 3625
Query 2035 CCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGTCTGGAAGGTGCTACT 2094
          |||
Sbjct 3626 CCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGTCTGGAAGGTGCTACT 3685
Query 2095 CCAGTGGCCACCAGCCTTGTCCTAATAAAATTAAGTTGCATCATTTTGTTTACTAGGTG 2154
          |||
Sbjct 3686 CCAGTGGCCACCAGCCTTGTCCTAATAAAATTAAGTTGCATCATTTTGTTTACTAGGTG 3745
Query 2155 TCCTTGATAATATTATGAGGGTGGAGGCGGGTGGTATGGAGCAAGGGGCCAGGTTGGGAA 2214
          |||
Sbjct 3746 TCCTTGATAATATTATGAGGGTGGAGGCGGGTGGTATGGAGCAAGGGGC-AGGTTGGGAA 3804
Query 2215 GACAACCTGTAGGGCCTTCAGGGTCTATTGCGGAACCAGGCTGGAGTGCAGTGGCA-G-T 2272
          |||
Sbjct 3805 GACAACCTGTAGGGCCTTCAGGGTCTATT-GGGAACCAGGCTGGAGTGCAGTGGCACGAT 3863
Query 2273 CTGGGCTCGCTGCAATCTCCGCTCCTGGGTTCAAGCGATTCTCTGCCAGCTCCTCCG 2332
          |||
Sbjct 3864 CTGGGCTCGCTGCAATCTCCGCTCCTGGGTTCAAGCGATTCTCTGCCAGCTCCTCCG 3923
Query 2333 AATAGTTCGCGATTCCAGGCATGCAAGACCAGGCTCAGCTAAATTTTGTATTTTGGTAGA 2392
          |||
Sbjct 3924 AATAGTTCGCGATTCCAGGCATGCAAGACCAGGCTCAGCTAAATTTTGTATTTTGGTAGA 3983
Query 2393 GACGGGGTTTACCATATTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCGCC 2452
          |||
Sbjct 3984 GACGGGGTTTACCATATTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCGCC 4043
Query 2453 CGCCTCGGCCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGGCCCTTCCCTGTCC 2512
          |||
Sbjct 4044 CGCCTCGGCCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGGCCCTTCCCTGTCC 4103
Query 2513 TGTGATTTTAAAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGCTACCTGG 2572
          |||
Sbjct 4104 TGTGATTTTAAAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGCTACCTGG 4163
Query 2573 CCATGCCAGCCAGTTGGACATTTGAGTTGTTGCTTGGCACTGTCTCTCATGCAATTGG 2632
          |||
Sbjct 4164 CCATGCCAGCCAGTTGGACATTTGAGTTGTTGCTTGGCACTGTCTCTCATGCAATTGG 4223
Query 2633 GTCCACTCAGTAGATGCTTGTGAATTC 2660
          |||
Sbjct 4224 GTCCACTCAGTAGATGCTTGTGAATTC 4251

Score = 204 bits (110), Expect = 4e-49
Identities = 213/261 (81%), Gaps = 14/261 (5%)
Strand=Plus/Plus

Query 2250 CCAGGCTGGAGTGCAGT-G-GCAGTCTTGGCTCGCTGCAATCTCCGCTCCTGGGTTCAA 2307
          |||
Sbjct 646 CCAGGCTGGAGTGCAGTGGCGCAATCTTGGCTCACAGCAACCTCTGCCTCCTGGGTTCAA 705
Query 2308 GCGATTCTCTGCCCTAGTCTCCCGAA-TAGTTGCGATTCCAGGCA--TGCAAGACCAGG 2364

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Sbjct	2127	AGCTCACCTAGCGCAATGGCTGCAGGTAAGCGCCCCATAAAATCCCTTTGGGCAACAATGT	2186
Query	599	GTCTTGAGGGGAGAGGCGCGTCTCTGTAGATGGGACGGGGGCACTAACCCCTCAGGTTTGG	658
Sbjct	2187	GTCTTGAGGGGAGAGGCGCGTCTCTGTAGATGGGACGGGGGCACTAACCCCTCAGGTTTGG	2246
Query	659	GGCTTATGAATGTTAGTATCGCCATCTAAGCCCAAGTATTGGCCAAATCTCTGAATGTT	718
Sbjct	2247	GGCTTATGAATGTTAG-TATCGCCATCTAAGCCCAAGTATTGGCCAAATCTCTGAATGTT	2305
Query	719	CTGGTCCCTGGA-GGAGGCagagagagagagagagagagagaaaaaaCCAGCTCTTGAAAC	777
Sbjct	2306	CTGGTCCCTTGAGGGAGGCAGAGAGAGAGAGAGAGAGAGAGAAAAAAACCAGCTCTTGAAAC	2365
Query	778	AGGGAGAGCGCTGGCCCTCTTGCTCTCCAGCTCCCTCTGTTGCCTCCGGTTTCTCCCCAGG	837
Sbjct	2366	AGGGAGAGCGCTGGCCCTCTTGCTCTCCAGCTCCCTCTGTTGCCTCCGGTTTCTCCCCAGG	2425
Query	838	CTCCCGGACGTCCTGCTCTGGCTTTTGGCTGCTCTGCCTGTCTGGCTTCAAGAGGG	897
Sbjct	2426	CTCCCGGACGTCCTGCTCTGGCTTTTGGCTGCTCTGACTGTCTGGCTTCAAGAGGG	2485
Query	898	CAGTGCCTTCCCAACCAATCCCTTATCCAGGCTTTTTGACAACGCTATGCTCCGCGCCG	957
Sbjct	2486	CAGTGCCTTCCCAACCAATCCCTTATCCAGGCTTTTTGACAACGCTATGCTCCGCGCCG	2545
Query	958	TCGCCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAAAGCTCTTGGGTAATGGG	1017
Sbjct	2546	TCGCCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAAAGCTCTTGGGTAATGGG	2605
Query	1018	TGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCTGGGAAGTAATGGGAGGAGA	1077
Sbjct	2606	TGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCTGGGAAGTAATGGGAGGAGA	2665
Query	1078	CTAAGGAGCTCAGGGTGTGTTTTCTGAAGTGAAAATGCAGGCAGATGAGCATACGCTGAGT	1137
Sbjct	2666	CTAAGGAGCTCAGGGTGTGTTTTCTGAAGTGAAAATGCAGGCAGATGAGCATACGCTGAGT	2725
Query	1138	GAGGTTCAGAAAAGTAACAATGGGAGCAGGTCTCCAGCATAGACCTTGGTGGGCGGTC	1197
Sbjct	2726	GAGGTTCAGAAAAGTAACAATGGGAGCTGGTCTCCAGCATAGACCTTGGTGGGCGGTC	2785
Query	1198	CTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTATTCTTGCAGAACCC	1257
Sbjct	2786	CTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTATTCTTGCAGAACCC	2845
Query	1258	CCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAACGCA	1317
Sbjct	2846	CCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAACGCA	2905
Query	1318	GCAGAAATCTGTAGTGGATGCCTTCTCCCCAGGTGGGATGGGTAGACCTGTGGTCAGA	1377
Sbjct	2906	GCAGAAATCTGTAGTGGATGCCTTCTCCCCAGGTGGGATGGGTAGACCTGTGGTCAGA	2965
Query	1378	GCCCCGGGAGCACAGCCACTGCCGCTCTTCCCTTCGAGAACCTAGAGCTGTCTCCGA	1437
Sbjct	2966	GCCCCGGGAGCACAGCCACTGCCGCTCTTCCCTTCGAGAACCTAGAGCTGTCTCCGA	3025
Query	1438	TCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCGTCGAGCTCCTCAGGAGCGTCTTCG	1499

Sbjct	3026	 TCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGAGCTCCTCAGGAGCGTCTTCG	3085
Query	1498	CCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGCTCTATCGCCACCTGAAGGACCTAG	1557
Sbjct	3086	 CCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGCTCTATCGCCACCTGAAGGACCTAG	3145
Query	1558	AGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAGG-ATCC--AATCTGGGG	1614
Sbjct	3146	AGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAGGGATCCCCAATCTCGGG	3205
Query	1615	CCCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTCTTTTATGAGTCAGG	1674
Sbjct	3206	CCCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTCTTTTATGAGTCAGG	3265
Query	1675	CGCTGACCCAAGAGAACTACCGTATTCTTCAATTTCCCTCGTGAATCTCCAGGCTTT	1734
Sbjct	3266	CGCTGACCCAAGAGAACTACCGTATTCTTCAATTTCCCTCGTGAATCTCCAGGCTTT	3325
Query	1735	CTCTACAACCTGGAGGGGAGGGAGGAAAATGGATGAATGAGAGGGGAGGGAACAGTGCC	1794
Sbjct	3326	CTCTACAACCTGGAGGGGAGGGAGGAAAATGGATGAATGAGAGGGGAGGGAACAGTGCC	3385
Query	1795	CAAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTTGAGAGGGCTGGAAGATGGCAGCCCC	1854
Sbjct	3386	CAAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTTGAGAGGGCTGGAAGATGGCAGCCCC	3445
Query	1855	CGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAAATCGCACAAAGAT	1914
Sbjct	3446	CGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAAATCGCACAAAGAT	3505
Query	1915	GACGCACTGCTCAAGAACTACGGGCTGCTACTGCTTCAGGAAGGACATGGACAAGGTC	1974
Sbjct	3506	GACGCACTGCTCAAGAACTACGGGCTGCTACTGCTTCAGGAAGGACATGGACAAGGTC	3565
Query	1975	GAGACATTCCTGCGCATCGTGCACTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGCTG	2034
Sbjct	3566	GAGACATTCCTGCGCATCGTGCACTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGCTG	3625
Query	2035	CCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCCTCTCCTGGTCTGGAAGGTGCTACT	2094
Sbjct	3626	CCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCCTCTCCTGGTCTGGAAGGTGCTACT	3685
Query	2095	CCAGTGCCCAACAGCCCTTGTCCTAATAAAATTAAGTTGCATCATTTTGTGTTGACTAGGTG	2154
Sbjct	3686	CCAGTGCCCAACAGCCCTTGTCCTAATAAAATTAAGTTGCATCATTTTGTGTTGACTAGGTG	3745
Query	2155	TCCTTGATAATATTATGAGGGTGGAGCGGGTGGTATGGAGCAAGGGGCCAGGTTGGGAA	2214
Sbjct	3746	TCCTTGATAATATTATGAGGGTGGAGCGGGTGGTATGGAGCAAGGGGC-AGGTTGGGAA	3804
Query	2215	GACAACCTGTAGGGCCCTCAGGGTCTATTTCGGGAACAGGCTGGAGTGCAGTGGCA-G-T	2272
Sbjct	3805	GACAACCTGTAGGGCCCTCAGGGTCTATT-GGGAACAGGCTGGAGTGCAGTGGCACGAT	3863
Query	2273	CTTGGCTCGTGCAATCTCCGCCTCTGGGTTCAAGCGATTCTCTGCCTCAGTCTCCCG	2332
Sbjct	3864	CTTGGCTCGTGCAATCTCCGCCTCTGGGTTCAAGCGATTCTCTGCCTCAGTCTCCCG	3923
Query	2333	AATAGTTGCGATTCCAGGCATGCAAGACCAGGCTCAGCTAATTTTGTATTTTGGTAGA	2392

Query	957	GTGCGCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAAAGCTCTTGGGTAATGG	1016
Sbjct	8150	GTGCGCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAAAGCTCTTGGGTAATGG	8091
Query	1017	GTGCGCTTACAGAGTGGCAGGAAGGGGTGAATTTCCCCCGCTGGGAAGTAATGGGAGGAG	1076
Sbjct	8090	GTGCGCTTACAGAGTGGCAGGAAGGGGTGAMTTTCCCCCGCTGGGAAGTAATGGGAGGAG	8031
Query	1077	ACTAAGGAGCTCAGGGTTGTTTCTGAAGTGAAAATGCAGGCAGATGAGCATACGCTGAG	1136
Sbjct	8030	ACTAAGGAGCTCAGGGTTGTTTCTGAAGTGAAAATGCAGGCAGATGAGCATACGCTGAG	7971
Query	1137	TGAGGTTCCCGAGAAAAGTAACAATGGGAGCAGGCTCCAGCATAGACCTTGGTGGGCGGT	1196
Sbjct	7970	TGAGGTTCCCGAGAAAAGTAACAATGGGAGCWGGTCTCCAGCATAGACCTTGGTGGGCGGT	7911
Query	1197	CCTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTCTTCTGCAGAAC	1256
Sbjct	7910	CCTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTCTTCTGCAGAAC	7851
Query	1257	CCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAACGC	1316
Sbjct	7850	CCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACWGGGTGAAAACGC	7791
Query	1317	AGCAGAAATCTGTGAGTGGATGCCTTCTCCCCAGGT--GGGATGGGGTAGACCTGTGGTCA	1375
Sbjct	7790	AGCAGAAATCTGTGAGTGGATGCCTTCTCCCCAGGTGGGGATGGGGTAGACCTGTGGTCA	7731
Query	1376	GAGCCCCCGGGCAGCAGCAGCCACTGCCGGTCTTCCCCTGCAAGAACCTAGAGCTGCTCCG	1435
Sbjct	7730	GAGCCCCCGGGCAGCAGCAGCCACTGCCGGTCTTCCCCTGCAAGAACCTAGAGCTGCTCCG	7671
Query	1436	CATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGACGCTCCTCAGGAGCGTCTT	1495
Sbjct	7670	CATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGACGCTCCTCAGGAGCGTCTT	7611
Query	1496	CGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGCTCTATCGCCACCTGAAGGACCT	1555
Sbjct	7610	CGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGCTCTATCGCCACCTGAAGGACCT	7551
Query	1556	AGAGGAAGGATCCAAACGCTGATGTGGGTGAGGGTGGCACCA--GGAT--CCAATCTGG	1612
Sbjct	7550	AGAGGAAGGATCCAAACGCTGATGTGGGTGAGGGTGGCACCAAGGATCCCAATCTGG	7491
Query	1613	GGCCCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTCTTTTAGCAGTCA	1672
Sbjct	7490	GGCCCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTCTTTTAGCAGTCA	7431
Query	1673	GGCGTGACCCCAAGAGAAGTACCGTATTCTTCTATTTCCTCTCGTGAATCTCCAGGCCT	1732
Sbjct	7430	GGCGTGACCCCAAGAGAAGTACCGTATTCTTCTATTTCCTCTCGTGAATCTCCAGGCCT	7371
Query	1733	TTCTCTACAACCTGGAGGGGAGGGAGGAAAAATGGATGAATGAGAGAGGGAGGGAACAGTG	1792
Sbjct	7370	TTCTCTACAACCTGRAGGGGAGGGAGGAAAAATGGATGAATGAGAGAGGGAGGGAACAGTG	7311
Query	1793	CCCAAGCGTTGGCCTCTCCTTCTCTTCTTCACTTTGAGAGGCTGGAAGATGGCAGCC	1852
Sbjct	7310	CCCAAGCGTTGGCCTCTCCTTCTCTTCTTCACTTTGAGAGGCTGGAAGATGGCAGCC	7251

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Query 1853 CCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAATCGCACAAACG 1912
          |||
Sbjct 7250 CCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAATCGCACAAACG 7191

Query 1913 ATGACGCACTGCCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGCATGGACAAGG 1972
          |||
Sbjct 7190 ATGACGCACTGCCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGCATGGACAAGG 7131

Query 1973 TCGAGACATTCTTCGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGC 2032
          |||
Sbjct 7130 TCGAGACATTCTTCGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGC 7071

Query 2033 TGCCCGGGTGGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGTCGTGGAAGGTGCTA 2092
          |||
Sbjct 7070 TGCCCGGGTGGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGTCGTGGAAGGTGCTA 7011

Query 2093 CTCCAGTGCCCAACGAGCTTGTCTTAATAAAATAAGTTGCATCATTTTGTGTTGACTAGG 2152
          |||
Sbjct 7010 CTCCAGTGCCCAACGAGCTTGTCTTAATAAAATAAGTTGCATCATTTTGTGTTGACTAGG 6951

Query 2153 TGTCTTGTATAATAATTATGAGGGTGGAGGCGGGTGGTATGGAGCAAGGGGCCAGGTTGGG 2212
          |||
Sbjct 6950 TGTCTTGTATAATAATTATGAGGGTGGAGGCGGGTGGTATGGAGCAAGGGG-CAGGTTGGG 6892

Query 2213 AAGACAACCTGTAGGGGCTTCAGGGTCTATTTCGGGAACCAAGGCTGGAGTGCAGTGGCA-G 2271
          |||
Sbjct 6891 AAGACAACCTGTAGGGGCTTCAGGGTCTATT-TGGGAACCAAGGCTGGAGTGCAGTGGCAGC 6833

Query 2272 -TCTTGGCTCGCTGCAATCTCCGCCCTCCTGGGTTCAAGCGATTCTCCTGCCCTCAGTCTCC 2330
          |||
Sbjct 6832 ATCTTGGCTCGCTGCAATCTCCGCCCTCCTGGGTTCAAGCGATTCTCCTGCCCTCAGTCTCC 6773

Query 2331 CGAATAGTTTGCATATCCAGGCAATGCAAGACCAGGCTCAGCTAATTTTGTATTTTGGTA 2390
          |||
Sbjct 6772 CGAATAGTTTGGGATTCCAGGCAATGCAAGACCAGGCTCAGCTAATTTTGTATTTTGGTA 6713

Query 2391 GAGACGGGGTTTACCAATATTGGCCAGTCTGGTCTCCAATCTCCTGACCTCAGGTAATCCG 2450
          |||
Sbjct 6712 GAGACGGGGTTTACCAATATTGGCCAGTCTGGTCTCCAATCTCCTGACCTCAGGTAATCCG 6653

Query 2451 CCCGCCCTCGGCCCTCCCAAATGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCCCTGT 2510
          |||
Sbjct 6652 CCCGCCCTCGGCCCTCCCAAATGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCCCTGT 6593

Query 2511 CCTGTGATTTTAAAATAATTATACCAGCAGAAGGACGTCAGACACAGCATGGGCTACCT 2570
          |||
Sbjct 6592 CCTGTGATTTTAAAATAATTATACCAGCAGAAGGACGTCAGACACAGCATGGGCTACCT 6533

Query 2571 GGCCATGCCACGACAGTTGGACATTGTAGTTGTTTGTCTTGGCACTGTCCCTCTCATGCATT 2630
          |||
Sbjct 6532 GRCCATGCCACGACAGTTGGACATTGTAGTTGTTTGTCTTGGCACTGTCCCTCTCATGCATT 6473

Query 2631 GGGTCCACTCAGTAGATGCTTGTGAATTC 2660
          |||
Sbjct 6472 GGGTCCACTCAGTAGATGCTTGTGAATTC 6443

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Score = 1037 bits (561), Expect = 0.0
 Identities = 680/737 (92%), Gaps = 9/737 (1%)
 Strand=Plus/Minus


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Sbjct 194 CAGCTCCTGGAGCAGGGAGAGCGCTGGCCTCTTCTCTCCGGCTCCCTCCATTGCCCTCC 135

Query 824 GGTITCTCCCCAGGCTCCCGGACGTCCTGCTCCTGGCTTTTGGCTGCTCTGCCTGTCC 883
|||||
Sbjct 134 GGTITCTCCCCAGGCTCCCGGACGTCCTGCTCCTGGCTTTTGGCTGCTCTGCCTGTCC 75

Query 884 TGGCTTCAAGAGGGCAG-TGCCTTCCCAACCATTCCTTATCCAGGCTTTTTGACAACGC 942
|||||
Sbjct 74 TGGCTTCAAGAGG-CTGGTGCCGTCCAAACCGTTCCGTTATCCAGGCTTTTGTACCACGC 16

Query 943 TATGCTCC 950
|||||
Sbjct 15 TATGCTCC 8

Score = 209 bits (113), Expect = 8e-51
Identities = 213/260 (81%), Gaps = 12/260 (4%)
Strand=Plus/Minus

Query 2250 CCAGGCTGGAGTGCAGT-G-GCAGTCTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAA 2307
|||||
Sbjct 10049 CCAGGCTGGAGTGCAGTGGCGCAATCTTGGCTCACAGCAACCTCTGCCTCCTGGGTTCAA 9990

Query 2308 GCGATTCTCCTGCCTCAGTCTCCCGAA-TAGTTGCATTCCAGGCA--TGCAAGACCAGG 2364
|||||
Sbjct 9989 GCGATTCTCCTGCCTCAGCTCC--AAGTAGCTGGGATTACGGGCTCGTGCCA--CCATG 9933

Query 2365 CTCAGCTAATTTTGTATTTT-GGTAGAGACGGGGTTTACCATATTGGCCAGTCTGGT 2423
|||||
Sbjct 9932 CCCAGCTAATTTTGTATTTTAGG-AGAGATGGAGTTTTCGATGTGGGTAGCCTGGT 9874

Query 2424 CTC-CATCTCTGACCTCAGGTAATCCGCCCGCTCGGCCCTCCCAAATGTGGGATTAC 2482
|||||
Sbjct 9873 CTTGCA-CTCCTGACCTTAAGTGATCCACCACCTCAGCCTCCCAAAGTGCTGGGATTAT 9815

Query 2483 AGGTATGAGCCACTGGGCC 2502
|||||
Sbjct 9814 AGGCATGAGCCACCGTGCCC 9795

>emb|CS741885.1| Sequence 9881 from Patent WO2005083127
Length=58905

Score = 4684 bits (2536), Expect = 0.0
Identities = 2625/2670 (98%), Gaps = 16/2670 (0%)
Strand=Plus/Plus

Query 1 GAATTCAGCACTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCT 60
|||||
Sbjct 42593 GAATTCAGCACTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCT 42652

Query 61 TTTCCCAACACACACATTCTGCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG 120
|||||
Sbjct 42653 TTTCCCAACACACACATTCTGCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG 42712

Query 121 GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGGCCATCTCTGACA 180
|||||
Sbjct 42713 GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGG-CTATCTGACA 42771

Query 181 TCCTTCTCCGCTTCAGGTTGGCCACCATGGCTGCTGCCAGAGGCACCCACGTGACCC 240

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Sbjct	42772		TCCTTCTCCGCGTTTCAGGTTGGCCACCATGGCTGCTGCCAGAGGGCACCCACGTGACCC	42831
Query	241		TTAAAGAGAGGACAAAGTTGGGTGGTATCTCTGGCTGACATTCTGTGCACAACCCCTCACAA	300
Sbjct	42832		TTAAAGAGAGGACAAAGTTGGGTGGTATCTCT-GCTGACATTCTGTGCACAACCCCTCACAA	42890
Query	301		CGCTGGTGATGGTGGGAAGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTGTG	360
Sbjct	42891		CGCTGGTGATGGTGGGAAGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTGTG	42950
Query	361		GGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCATAACATG	420
Sbjct	42951		GGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCATAACATG	43010
Query	421		CAGAGAAACAGGTGAGGAGAAGCAGCGAGAGAGAAGGGGCCAGGTATAAAAGGGCCCCAC	480
Sbjct	43011		CAGAGAAACAGGTGAGGAGAAGCAGCGAGAGAGAAGGGGCCAGGTATAAAAGGGCCCCAC	43070
Query	481		AAGAGACCAGCTCAAGGATCCCAAGGCCCAACTCCCCGAACCTCAGGGTCTGTGGAC	540
Sbjct	43071		AAGAGACCAGCTCAAGGATCCCAAGGCCCAACTCCCCGAACCTCAGGGTCTGTGGAC	43130
Query	541		AGCTCA-CTAGCGGCAATGGCTGCAGGTAAGCGCCCCATAAATCCCTTT-GGCACAATGT	598
Sbjct	43131		AGCTCACCTAGCGGCAATGGCTGCAGGTAAGCGCCCCATAAATCCCTTTGGGACAAATGT	43190
Query	599		GTCTTGAGGGGAGAGGCGGCGTCTGTAGATGGGACGGGGGCACTAACCCCTCAGGTTTGG	658
Sbjct	43191		GTCTTGAGGGGAGAGGCGGCGTCTGTAGATGGGACGGGGGCACTAACCCCTCAGGTTTGG	43250
Query	659		GGCTTATGAATGTAGCTATCGCCATCTAAGCCCAAGTATTGTGCCAATCTCTGAATGTTT	718
Sbjct	43251		GGCTTATGAATGTAGTATCGCCATCTAAGCCCAAGTATTGTGCCAATCTCTGAATGTTT	43309
Query	719		CTGGTCCCTGGA-GGAGGCagagagagagagagagagagaaaaaaaaaCCAGCTCCTGGAAC	777
Sbjct	43310		CTGGTCCCTGAGGGGAGGC-AGAGAGAGAGAGAGARAAAAAAAAAACCCAGCTCCTGGAAC	43368
Query	778		AGGGAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTTG-CCTCCGGTTTCTCCCGAG	836
Sbjct	43369		AGGGAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTTGCGCCTCCGGTTTCTCCCGAG	43428
Query	837		GCTCCCGGACGCTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGCTCCTGGCTTCAAGAGG	896
Sbjct	43429		GCTCCCGGACGCTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGCTCCTGGCTTCAAGAGG	43488
Query	897		GCAGTGCCTTCCCAACCAATTCCCTTATCCAGGCTTTTGTGACAACGCTATGCTCCGCGCCC	956
Sbjct	43489		GCAGTGCCTTCCCAACCAATTCCCTTATCCAGGCTTTTGTGACAACGCTATGCTCCGCGCCC	43548
Query	957		GTCGCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAAAGCTCTTGGGTAATGG	1016
Sbjct	43549		GTCGCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAAAGCTCTTGGGTAATGG	43608
Query	1017		GTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCTGGGAAGTAATGGGAGGAG	1076
Sbjct	43609		GTGCGCTTCAGAGGTGGCAGGAAGGGGTGAMTTTCCCCCGCTGGGAAGTAATGGGAGGAG	43668
Query	1077		ACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAATAATGCAGGCAGATGAGCATACGCTGAG	1136


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Sbjct  44569  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 44628
TCGAGACATTCTCGGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGC

Query  2033  TGCCCGGGTGGCATCCCTGTGACCCCTCCCAAGTGCCTCTCTGGTCTGGAAGGTGCTA 2092
|||||

Sbjct  44629  TGCCCGGGTGGCATCCCTGTGACCCCTCCCAAGTGCCTCTCTGGTCTGGAAGGTGCTA 44688
|||||

Query  2093  CTCAGTGCCCAACAGCCCTTGTCCTAATAAAATTAAGTTGCATCAITTTTGTGTTGACTAGG 2152
|||||

Sbjct  44689  CTCAGTGCCCAACAGCCCTTGTCCTAATAAAATTAAGTTGCATCAITTTTGTGTTGACTAGG 44748
|||||

Query  2153  TGTCCTTGATAATAATTAATGAGGTGGAGGCGGGTGGTATGGAGCAAGGGGCGAGGTTGGG 2212
|||||

Sbjct  44749  TGTCCTTGATAATAATTAATGAGGTGGAGGCGGGTGGTATGGAGCAAGGGGCGAGGTTGGG 44807
|||||

Query  2213  AAGACAACCTGTAGGGCCTTCAGGGTCTATTTCGGGAACAGGCTGGAGTGCAGTGGCA-G 2271
|||||

Sbjct  44808  AAGACAACCTGTAGGGCCTTCAGGGTCTATT-GGGAACAGGCTGGAGTGCAGTGGCAGC 44866
|||||

Query  2272  -TCTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAGGCGATTCTCCTGCCTCAGTCTCC 2330
|||||

Sbjct  44867  ATCTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAGGCGATTCTCCTGCCTCAGTCTCC 44926
|||||

Query  2331  CGAATAGTTGCGATTCCAGGCATGCAAGACCAGGCTCAGCTAATTTTTGTATTTTTGGTA 2390
|||||

Sbjct  44927  CGAATAGTTGGGATTCCAGGCATGCACGACCAGGCTCAGCTAATTTTTGTATTTTTGGTA 44986
|||||

Query  2391  GAGACGGGGTTTACCATATTGGCCAGTCTGGTCTCCATCTCTGACCTCAGGTAATCCG 2450
|||||

Sbjct  44987  GAGACGGGGTTTACCATATTGGCCAGTCTGGTCTCCATCTCTGACCTCAGGTAATCCG 45046
|||||

Query  2451  CCCGCCTCGGCCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCCCTGT 2510
|||||

Sbjct  45047  CCCGCCTCGGCCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCCCTGT 45106
|||||

Query  2511  CCTGTGATTTTTAAAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGCTACCT 2570
|||||

Sbjct  45107  CCTGTGATTTTTAAAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGCTACCT 45166
|||||

Query  2571  GGCCATGCCAGCCAGTGGACATTTGAGTTGTTTGGCTTGGCACTGTCTCTCATGCATT 2630
|||||

Sbjct  45167  GRCCATGCCAGCCAGTGGACATTTGAGTTGTTTGGCTTGGCACTGTCTCTCATGCATT 45226
|||||

Query  2631  GGGTCCACTCAGTAGATGCTTGTGAATTC 2660
|||||

Sbjct  45227  GGGTCCACTCAGTAGATGCTTGTGAATTC 45256
|||||

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Score = 2760 bits (1494), Expect = 0.0
Identities = 1766/1908 (92%), Gaps = 19/1908 (0%)
Strand=Plus/Plus

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Query  765  CAGCTCCTGGAACAGGGAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTG-CCTCC 823
|||||

Sbjct  6412  CAGCTCCTGGAGCAGGAGAGYGTGGCCTCTTGCTCTCCGGCTCCCTCTGTGCCCCCTCT 6471
|||||

Query  824  GGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCC 883
|||||

Sbjct  6472  GGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGCC 6531
|||||

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Query	884	TGGCTTCAAGAGGGCAGTGCCTTCCCAACCAATTCCTTATCCAGGCTTTTGACAACGCT	943
Sbjct	6532	TGGCTTCAAGAGGGCAGTGCCTTCCCAACCAATTCCTTATCCAGGCTTTTGACAACGCT	6591
Query	944	ATGCTCCGCGCCCGTCGCCGTGACCAGCTGGCATAATGACACCTATCAGGAGTTTGTAAAGC	1003
Sbjct	6592	ATGCTCYGCGCCCATCGTCTGCACCAAGCTGGCMTWTGACAYCTACCAAGGAGTTTGTAAAGC	6651
Query	1004	TCTTGGGTAATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCTGGGAA	1063
Sbjct	6652	TCTTGGGGAATGGGTGCGCATCAGGGGTGGCAGGAAGGGGTGACTTTCCCCCGCTGGGAA	6711
Query	1064	GTAATG--GGAGGAGACTAAGGAGCTCAGGGTTGTTTCTGAAGTGAATAATGCAGGCAGAT	1122
Sbjct	6712	ATAA--GAGGAGGAGACTAAGGAGCTCAGGGTT--TTCCYGAAGCGAAAATGCAGGCAGAT	6769
Query	1123	GAGCATACGCTGAGTGAAGTTCCAGAAAAGTAACAATGGGAGCAGGTCTCCAGCATAGA	1182
Sbjct	6770	GAGCACACGCTGAGTGAAGTTCCAGAAAAGTAACAATGGGAGCTGGTCTCCAGCGTAGA	6829
Query	1183	CCTTGGTGGGCGGTCTCTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTC	1242
Sbjct	6830	CCTTGGTGGGCGGTCTCTCTCCTAGGAAGAAGCCTATATCCCAAAGGAACAGAAGTATTC	6889
Query	1243	ATTCTCTGAGAACCCCGAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAA	1302
Sbjct	6890	ATTCTCTGAGAACCCCGAGACCTCCCTCTGTTTCTCAGAGTCTATTCCGACACCTTCCAA	6949
Query	1303	CAGGGTGAAGAACGACGACGAGAAAT--CTGTGAGTGGATGCCTTCTCCCCAGG--TGGGATGGG	1360
Sbjct	6950	CAGGGAGGAAACACAAAGAAATY--GTGAGTGGATGCCTTCTCCCCAGCGGGGATGGG	7008
Query	1361	GTAGACCTGTGGTCAGAGCCCCGGGCAGCACAGCCACTGCGGTCCTTCCCTGCAGAA	1420
Sbjct	7009	GGAGACCTGTAGTCAGAGCCCCGGGCAGCACAGCCAAATGCCCGTCTTCCCTGCAGAA	7068
Query	1421	CCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCT	1480
Sbjct	7069	CCTARAGCTGCTCYGCATCTSCCTGCTGCTCATCCAGTCGTTGGCTGGAGCCCGTGCAGTT	7128
Query	1481	CCTCAGGAGCGCTCTTGCCCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGCTCTATCG	1540
Sbjct	7129	CCTCAGGAGTGTCTTGCCCAACAGCCTGGTGTACGGCGCCTCTGACWGCAACDCTAT--G	7187
Query	1541	--CCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCA--	1598
Sbjct	7188	RCCTCTCTAAAGGACCTAGAGGAAGGCATCCAAACRCTGATGGGGGTGAGGGTGGCGCCAG	7247
Query	1599	GGAT--CCAATCCTGGGGCCCCACTGGCTTCCAGGGAGCTG--GGGAGAGAAACACTGTGTC	1655
Sbjct	7248	GGKTCGCCAATCCTGGAGCCCCACTGACTTTGAGAG--CTGTRTTAGAGAAACACTGTGTC	7306
Query	1656	CCTCTTTTTAGCAGTCAGGCGCTGACCCAAAGAGAACTACCGTATTCTTCATTTCCCTC	1715
Sbjct	7307	CCTCTTTTTAGCAGWAGGCGCTGACCCAAAGAGAACTACCTTATTCTTCATTTCCCTC	7366
Query	1716	GTGAATCCTCAGGCCCTTCTCTACAACCTGGAGGGGAGGGAGGAAAAATGGATGAATGAG	1775
Sbjct	7367	RTGAATCCTCAGGCCCTTCTCTACAACCTGAAGGGGAGGGAGGAAAAATGAATGAATGAG	7426

Score = 1940 bits (1050), Expect = 0.0
 Identities = 1367/1518 (90%), Gaps = 39/1518 (2%)
 Strand=Plus/Plus

Query	765	CAGCTCCTGGAACAGGGAGAGCGCTGGCCCTCTTGTCTCTCCAGCTCCCTCTGTTG-CCTCC	823
Sbjct	28671	CAGCTCCTGGAACAGGGAGAGCGCTGGCCCTCTTGTCTCTCCAGCTCCCTCTGTTG-CCTCC	28730
Query	824	GGTTTCTCCCGAGGCTCCCGGACGTCCTGCTCCTGGCTTTTGGCCCTGCTCTGCGCTGTC	883
Sbjct	28731	GGTTTCTCCCGAGGCTCCCGGACGTCCTGCTCCTGGCTTTTGGCCCTGCTCTGCGCTGTC	28790
Query	884	TGGCTTCAAGAGGGC-AGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTGTGACAAACGC	942
Sbjct	28791	TGGCTTCAAGA-GGCTGGTGCCGTCCTCAACCGTTCGTTATCCAGGCTTTTGTGACAAACGC	28849
Query	943	TATGCTCCGCGCCCGTCGC-CTGTACCAGCTGG-CATATGACACCTATCAGGAGTTTGTA	1000
Sbjct	28850	TATGCTCCAAGCCCATCGCGC-GCACCAGCTGGCCAT-TGACACCTACCAGGAGTTTGTA	28907
Query	1001	AGTCTCTGGGTAAATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCT-G	1059
Sbjct	28908	AGTTCTTGGGGAATGGGTGCGGGTCAGGGGTGGCAAGAAGGGGTGACTTTCCCCCACTGG	28967
Query	1060	GGAAGTAATGGGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAATGCAGGCA	1119
Sbjct	28968	GGAAGTAATGGGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAATGCAGGCA	29027
Query	1120	GATGAGCATACGCTGAGTGAGGTCCCGAGAAAAGTAACAATGGGAGCAGGTCTCCAGCAT	1179
Sbjct	29028	GATGAGCATAGGCTGAGCCAGGTTCCTCAGAAAAGCAACAATGGGAGCTGGTCTCCAGCAT	29087
Query	1180	-----AG-A---C--CTTGGTGGGCGGTCTTCTCCTAGGAAGAAGCCTATATCTGA	1226
Sbjct	29088	AGAAACCAGCAGTCTTCTTGGTGGGGGTCTTCTCCTAGGAAGAAGCCTATATCCCAA	29147
Query	1227	AGGAGCAGAAGTATTCTTCCTGCA-GAACCCCGAGACCTCCCTCTGCTTCTCAGAGTCT	1285
Sbjct	29148	AGGACCAGAAGTATTCTTCCTGCATG-ACTCCAGACCTCCTTCTGCTTCTCAGACTCT	29206
Query	1286	ATTCCAACACCTTCCAACAGGGTGAAAACGACGAGAAATCTGTGAGTGGATGCCCTTCTC	1345
Sbjct	29207	ATTCCGACACCTTCCAACATGGAGGAACGCAACGAGAAATCCGTGAGTGGATGCCCTTCTC	29266
Query	1346	CCC-AGG-TGGGATGGGGTAGACCTGTGGTCAGAGCCCCGGGCGAGCAGCCACTGCGC	1403
Sbjct	29267	CCCTAGGCGGGGATGGGGGAGACCTGTGGTCAGGGCTCCCGGCGAGCAGCCACTGCGC	29326
Query	1404	GTCTTCCCTTCGAGAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGG	1463
Sbjct	29327	GTCTTCCCTTCGAGAACTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCGAGTCGTGG	29386
Query	1464	CTGGAGCCCGTCGAGCTCCTCAGGAGCGTCTTCGCAACAGCCTGGTGTATGGCGCCTCG	1523
Sbjct	29387	CTGGAGCCCGTCGCGGTCTCCTCAGGAGTATGTTTCGCAACAACTGGTGTATGACACCTCG	29446
Query	1524	GACAGCAACGCTCTATCGCCACCTGAAGGACCTAGAGGAAGGCATCCAACAGCTGATGTGG	1583
Sbjct	29447	GACAGCGATGACTATCACCTCTAAAGGAGCTAGAGGAAGGCATCCAACAGCTGATGGG	29506

Sbjct	51565	GGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGCCCTGCTCTGCCTGCC	51624
Query	884	TGGCTTCAAGAGGGC-AGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGTACAACGC	942
Sbjct	51625	TGGCTTCAAGA-GGCTGGTGCCCTCCAAACCGTTCGGTATCCAGGCTTTTGACCACGC	51683
Query	943	TATGCTCCGCGCCCGTCGC-CTGTACCAGCTGG-CATATGACACCTATCAGGAGTTTGTA	1000
Sbjct	51684	TATGCTCCAAGCCCATCGCGC-GCACAGCTGGCCAT-TGACACCTACCAGGAGTTTGTA	51741
Query	1001	AGTCTTGGGTAAATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCT-G	1059
Sbjct	51742	AGTTCTTGGGGAATGGGTGCGGGTCAGGGGTGGCAAGAAGGGGTGACTTTCCCCCACTGG	51801
Query	1060	GGAAGTAATGGGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAATGCAGGCA	1119
Sbjct	51802	GGAAGTAATGGGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGCGAAATGCAGGCA	51861
Query	1120	GATGAGCATACGTGAGTGAGTTCCAGAAAAGTAACAATGGGAGCAGGTCTCCAGCAT	1179
Sbjct	51862	GATGAGCATAGGCTGAGCCAGGTTCCAGAAAAGCAACAATGGGAGCTGGTCTCCAGCAT	51921
Query	1180	-----AG-A---C--CTTGGTGGGCGGTCCTTCTCTAGGAAGAAGCCTATATCTGA	1226
Sbjct	51922	AGAAACAGCAGTCCTTCTTGGTGGGGGTCCTTCTCTAGGAAGAAGCCTATATCCAA	51981
Query	1227	AGGAGCAGAAGTATTCATTCTGCA-GAACCCCGAGACCTCCCTCTGCTTCTCAGAGTCT	1285
Sbjct	51982	AGGACCAGAAGTATTCATTCTGCACTG-ACCTCCAGACCTCCTTCTGCTTCTCAGACTCT	52040
Query	1286	ATTCACACACCTTCCAAACAGGTGAAAACGACGAGAAATCTGTGAGTGGATGCCCTTCTC	1345
Sbjct	52041	ATTCGACACCTTCCAAACATGGAGGAACGCAACAGAAATCCGTGAGTGGATGCCGTCTC	52100
Query	1346	CCC-AGG-TGGGATGGGGTAGACCTGTGGTCAGAGCCCCGGGCGAGCACGCCACTGCCG	1403
Sbjct	52101	CCCTAGGCGGGATGGGGGAGACCTGTGGTCAGGGCTCCCGGGCGAGCACGCCACTGCCG	52160
Query	1404	GTCTTCCCTTCGAGAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGG	1463
Sbjct	52161	GTCTTCCCTTCGAGAACTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCGAGTCGTGG	52220
Query	1464	CTGGAGCCCGTCGAGCTCCTCAGGAGCGTCTTCGCCAACAGCCTGGTGTATGGCGCTCG	1523
Sbjct	52221	CTGGAGCCCGTCGCGGTTCTCAGGATATGTTGCCAACAACTGGTGTATGACACCTCG	52280
Query	1524	GACAGCAACGCTATCGCCACCTGAAGGACCTAGAGGAAGGCATCCAACGCTGATGTGG	1583
Sbjct	52281	GACAGCGATGACTATCACTCTCAAAGGACCTAGAGGAAGGCATCCAACGCTGATGGGG	52340
Query	1584	GTGAGGGTGGCACCA-GGAT--CCAATCTGGGGCCCCACTTGCTTCCAGGGACT-GGGG	1639
Sbjct	52341	GTGAGGGTGGCGCCAGGGGTCGCCAATCTGGAAACCCACTTGCTTMMAGGG-CTGGGGG	52399
Query	1640	AGAGAAACACTGCTGCCCTCTTTTAGCAGTCAGGCGCTGACCCAAGAGAACTCACCGTA	1699
Sbjct	52400	AGAGAAAYACTGCTGCCCTCTTTTAGCAGTMAGGCGCTGACCCAAGAGAACTCACCTTA	52459
Query	1700	TTCTTCATTTCCCTCGTGAACTCTCCAGGCTTTCTCTACAACCTGGAGGGGAGGGAGG	1759

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Sbjct 52460 TTCTTCATTTCGCCTGGTGAATCCTCCAGGCCYTTCTCTACACCCTGAAGGGGAGGGAGG 52519
Query 1760 AAAATGGATGAATGAGAGAGGGGAGGGAACAGTGCCCAAGCGCTTGGCCCTCTCCTTCTCTT 1819
Sbjct 52520 AAAATGGATGAATGAGAGAGGGGAGGGAACAGTGCCCAAGCGCTTGGCCCTCTCCTTCTCTT 52579
Query 1820 CCTTCACCTTTGCAGAGGCTGGAAGATGGCAGCCCCGGGACTGGGCAGATCTTCAATCAGT 1879
Sbjct 52580 CCTTCACCTTTGCAGAGGCTGGAAGACGGCAGCCGGGACTGGGCAGATCTCTCAAGCAGA 52639
Query 1880 CCTACAGCAAGTTTGACACAAAATCGCACAAACGATGACGCACTGCTCAAGAACTACGGGC 1939
Sbjct 52640 CCTACAGCAAGTTTGACACAAAATTCRCACAACCATGACGCACTGCTCAAGAACTACGGGC 52699
Query 1940 TGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTCGCGCATCGTGCAGT 1999
Sbjct 52700 TGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTCGCGCATCGTGCAGT 52759
Query 2000 GCCGCTCTGTGGAGGGGAGCTGTGGCTTCTAGCTGCCCGGTGGCATCCCTGTGACC--C 2057
Sbjct 52760 GCCGCTCTGTAGAGGGTAGCTGTGGCTTCTAGGTGCCCGGTGGCATCC--TGTGACCGAC 52818
Query 2058 C--TCCCCAGTGCCTCTCTGGTCGTGGAAGGTGCTACTCCAGTGCCACCAGCCTTGTC 2115
Sbjct 52819 CCCCTCCCAGTGCCTCTCTGGCCCTGGAAGGTGCCACTCCAGTGCCCATCAGCCTTGTC 52878
Query 2116 CTAATAAAATTAAGTTGCATCATTTTGTGTGACTAGGTGTCCTTGTATAATATTATGGGG 2175
Sbjct 52879 CTAATAAAATTAAGTTGTATCATTTCTGACTAGGTGTCATTCTATAATATTATGGGG 52938
Query 2176 TGGA--GGCGGGTGGTATGGAGCAAGGGGCCAGGTTGGGAAGACA--ACCTGTAGGGCCTTC 2233
Sbjct 52939 TGGAAGGTGG--TGGTATGGAGCAAGGGGT--AGGT--GGAAAGA--AGACCTGAGGGCCTTC 52994
Query 2234 AGGGTCTATTTCGGGAACGAGC 2255
Sbjct 52995 AAGRTCTATT--GGGAAC TAGGC 53015

Score = 1879 bits (1017), Expect = 0.0
Identities = 1359/1522 (89%), Gaps = 48/1522 (3%)
Strand=Plus/Plus

Query 765 CAGCTCCTGGAACAGGGAGAGCGCTGGCCCTCTTGCTCTCCAGCTCCCTCTGTG--CCTCC 823
Sbjct 13985 CAGCTCCTGGAACAGGGAGAGTGTGCTGGCCCTCTTGCTCTGCGGCTCCCT--TCTTGCCCTCC 14043
Query 824 GGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCGTGTCC 883
Sbjct 14044 GGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCGTGTCC 14103
Query 884 TGGCTTCAAGAGGGC--AGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTTTGACA--ACG 941
Sbjct 14104 TGGCTTCAAGA--GGCTGGTGCCGTCCAAACCGTTCCTTATCCAGGCTTTTT--AAAGAGG 14161
Query 942 CTATGCTCCGCGCCCGTGC--CTGTACCAGCTGG--CATATGACACCATACAGGAGTTTGT 999
Sbjct 14162 CTATGCTCCAAGCCCATCGCGC--ACACCAGCTGGCCAT--TGACACCTACCAGGAGTTTAT 14219
Query 1000 AAGCTCTTGGGTAATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCGCGCT-- 1058

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Query	1	GAATTCAGCACTGAATCATGTGCCAGAACCCCCGCAATCTATTGGCTGTGCTTTGGCCCTT	60
Sbjct	13231	GAATTCAGGAGCTGAATCATGTGCTCAACCCCCACAATCTATTGGCTGTGC-TTGGCCCTT	13289
Query	61	TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAATCGCGGGAGGAGGAAAG	120
Sbjct	13290	TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGTAAACATCGCGGGAGGAGGAAAG	13349
Query	121	GAATAGGATAGAGAGTGGGATGGGGTCGTAGGGGTCTCAAGGACTGGCCTATCCTGACA	180
Sbjct	13350	GAATAGGATAGAGAGTGGGATGTGGTCGATAGGGGTCTCAAGGACTGG-CTATCCTGACA	13408
Query	181	TCCTTCTCCGCGTTTCAGGTTGGCCACCATTGGCTGCTGCCAGAGGGCACCCACGTGACCC	240
Sbjct	13409	TCCTTCTCCKCAITTCAGGTTGGCCACCATTGGCTGCTGCCAGAGGGCACCCACCTGAACC	13468
Query	241	TTAAAGAGAGGACAAAGTTGGGTGGTACTCTTGCTGACATTCTGTGCACAACCCCTACAA	300
Sbjct	13469	TTAAAGAGAGGACAAAGTTGGGTGGTCTCTGTGGTTGACACTCTGTGCACAACCCCTACAA	13528
Query	301	CGCTGGTGATGGTGGGAAGGGAAAGATGACAAGTCAGGGGGCATGATCCAGCATGTGTG	360
Sbjct	13529	CGCTGGTGACGGTGGGAAGGGAAAGATGACAAGCCAGGGGACATGATGCCAGCATGTGTG	13588
Query	361	GGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCTAAACATG	420
Sbjct	13589	GGAGGAGCTTCCAAATTATCCATTAGCACAGCCCGTCAGTGGCCCCATGCATAAATGTG	13648

3/2/09


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Query   2365   CTCAGCTAATTTTGTATTTT-GGTAGAGACGGGGTTTCACCATAATTGGCCAGTCTGGT   2423
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct   41767   CCCAGCTAATTTTGTATTTTAGG-AGAGATGGAGTTTGGCCATGTGGGTTAGCCTGGT   41825

Query   2424   CTC-CATCTCCTGACCTCAGGTAATCCGCCCGCCCTCGGCCCTCCCAAATGTCTGGGATTAC   2482
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct   41826   CTTCGA-CTCCTGACCTTAAGTGATCCACCACCTCAGCCTCCCAAAGTGCTGGGATTAT   41884

Query   2483   AGGTAIGAGCCATGGGCC   2502
          ||| | | | | | | | | |
Sbjct   41885   AGGCATGAGCCACCGTGCCC   41904

>gb|GC699295.1| Sequence 14540 from patent US 6812339
Length=5692

Score = 2802 bits (1517), Expect = 0.0
Identities = 1780/1907 (93%), Gaps = 17/1907 (0%)
Strand=Plus/Plus

Query   765   CAGTCTCTGGAACAGGGAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTTG-CCITCC   823
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct   2313   CAGTCTCTGGAGCAGGGAGAGTGCTGGCCTCTTGCTCTCCGGCTCCCTCTGTTGCCCTCT   2372

Query   824   GGTTTCTCCCCAGGCTCCCGGACGTCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCC   883
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct   2373   GGTTTCTCCCCAGGCTCCCGGACGTCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCC   2432

Query   884   TGGCTTCAAGAGGGCAGTGCCCTCCCAACCATTCCTTTATCCAGGCTTTTTGACAACGCT   943
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct   2433   TGGCTTCAAGAGGGCAGTGCCCTCCCAACCATTCCTTTATCCAGGCTTTTTGACAACGCT   2492

Query   944   ATGCTCCGCGCCCGTCGCCGTGACCAGCTGGCATATGACACCTATCAGGAGTTTGTAAAGC   1003
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct   2493   ATGCTCCGCGCCCATCGTCTGCACAGCTGGCCTTTGACACCTACCAGGAGTTTGTAAAGC   2552

Query   1004   TCTTGGGTAATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCTGGGAA   1063
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct   2553   TCTTGGGGAATGGGTGCGCATCAGGGGTGGCAGGAAGGGGTGACTTTCCCCCGCTGGGAA   2612

Query   1064   GTAATG-GGAGGAGACTAAGGAGCTCAGGGTTGTTTTCGTAAGTGAATAATGCAGGCAGAT   1122
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct   2613   ATAA-GAGGAGGAGACTAAGGAGCTCAGGGTT-TTCCCGAAGCGAAAATGCAGGCAGAT   2670

Query   1123   GAGCATACGCTGAGTGAGGTTCCAGAAAAGTAACAATGGGAGCAGGTCTCCAGCATAGA   1182
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct   2671   GAGCACACGCTGAGTGAGGTTCCAGAAAAGTAACAATGGGAGCTGCTTCCAGGCTAGA   2730

Query   1183   CCTTGGTGGGCGGTCCTTCTCCTAGGAAGAAGCCTATATCTGAAGGAGCAGAAATATTC   1242
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct   2731   CCTTGGTGGGCGGTCCTTCTCCTAGGAAGAAGCCTATATCCCAAAGGAACAGAAATATTC   2790

Query   1243   ATTCTCTGAGAACCCCGAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAA   1302
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct   2791   ATTCTCTGAGAACCCCGAGACCTCCCTCTGTTTCTCAGAGTCTATTCCGACACCTTCCAA   2850

Query   1303   CAGGGTGAAAACGCAGCAGAAAATCTGTGAGTGGATGCTTCTCCCCAGG-TGGGATGGGG   1361
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct   2851   CAGGGAGGAAAACACAGAAAATCCGTGAGTGGATGCTTCTCCCCAGGCGGGGATGGGG   2910

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Query	1362	TAGACCTGTGGTCAGAGCCCCGGGCAGCACAGCCACTGCCGGTCTTCCCTGCAGAAC	1421
Sbjct	2911	GAGACCTGTAGTCAGAGCCCCGGGCAGCACAGCCAATGCCCGTCTTCCCTGCAGAAC	2970
Query	1422	CTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTCAGCTC	1481
Sbjct	2971	CTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTCAGTTT	3030
Query	1482	CTCAGGAGCGTCTTCGCCAACAGCGCTGGTGTAAGCGCCTCGGACAGCAACGCTCTATCG-	1540
Sbjct	3031	CTCAGGAGTGCTCTTCGCCAACAGCGCTGGTGTAAGCGCCTCTGACAGCAACGCTCTAT-GA	3089
Query	1541	CCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCA-G	1599
Sbjct	3090	CCTCCTAAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCCAGG	3149
Query	1600	GAT--CCAATCTCTGGGGCCCCACTGGCTTCAGGGACTG-GGGAGAGAAACACTGCTGCC	1656
Sbjct	3150	GGTCCCCAATCTCTGGAGCCCCACTGACTTTGAGAG-CTGTGTTAGAGAAACACTGCTGCC	3208
Query	1657	CTCTTTTATAGAGTCAGGCGCTGACCCAAGAGAAGTACCCGATTTCTTCTATTCCCTCG	1716
Sbjct	3209	CTCTTTTATAGAGTCAGGCGCTGACCCAAGAGAAGTACCTTATTCTTCTATTCCCTCG	3268
Query	1717	TGAATCCTCCAGGCGCTTCTCTACAACTGGAGGGGAGGAGGAAAATGGATGAATGAGA	1776
Sbjct	3269	TGAATCCTCCAGGCGCTTCTCTACAACTGGAGGGGAGGAGGAAAATGAATGAATGAGA	3328
Query	1777	GAGGGAGGGAACAGTGCCTAAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTTGAGAGG	1836
Sbjct	3329	AAGGGAGGGAACAGTGCCTAAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTTGAGAGG	3388
Query	1837	CTGGAAGATGGCAGCCCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGAC	1896
Sbjct	3389	CTGGAAGATGGCAGCCCCGGACTGGGCAGATCTTCAAGCAGACTACAGCAAGTTTGAC	3448
Query	1897	ACAAAAATCGCAACACGATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGG	1956
Sbjct	3449	ACAAACTCACACAACGATGACGCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGG	3508
Query	1957	AAGGACATGGACAAGGTCGAGACATTCTCGGCATCGTCAGTGCCGCTCTGTGGAGGGC	2016
Sbjct	3509	AAGGACATGGACAAGGTCGAGACATTCTCGGCATCGTCAGTGCCGCTCTGTGGAGGGC	3568
Query	2017	AGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTGTGACCCCTCCCGATGCCTCTCCTG	2076
Sbjct	3569	AGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTGTGACCCCTCCCGATGCCTCTCCTG	3628
Query	2077	GTCGTGGAAGGTGCTACTCCAGTGCCCAACAGCCTTGTCTTAATAAAATTAAGTTGCATC	2136
Sbjct	3629	GCCCTGGAAGTTGCCACTCCAGTGCCCAACAGCCTTGTCTTAATAAAATTAAGTTGCATC	3688
Query	2137	ATTTTGTGTTGACTAGGTGTCTTGTATAATATTATGGGGTGGAGGCGGGTGGTATGGAGC	2196
Sbjct	3689	ATTTTGTGTTGACTAGGTGTCTTGTATAATATTATGGGGTGGAGGCGGGTGGTATGGAGC	3748
Query	2197	AAGGGGCCAGGTGTGGGAAGACAACCTGTAGGGCCTTCAGGGTCTATTTCGGGAACCAAGCT	2256
Sbjct	3749	AAGGGGCAAG-TTGGGAAGACAACCTGTAGGGCCTGCGGGTCTATT-GGGAACCAAGCT	3806

Query	2257	GGAGTGCAGTGGCAG--TCTTGGCTCGCTGCAATCTCCGCCTCTCTGGGTTCAAGCGATTCT	2314
Sbjct	3807	GGAGTGCAGTGGCACAATCTGGCTACTGCAATCTCCGCCTCTCTGGGTTCAAGCGATTCT	3866
Query	2315	TCCTGCCTCAGTCTCCCGAATAGTTGCGATTCCAGGCATGCAAGACCAGGCTCAGCTAAT	2374
Sbjct	3867	TCCTGCCTCAGCCTCCCGAGTTGTTGGGATTCCAGGCATGCATGACCAGGCTCAGCTAAT	3926
Query	2375	TTTTGTATTTTTGGTAGAGACGGGGTTTCACCATATTGGCCAGTCTGGTCTCCATCTCCT	2434
Sbjct	3927	TTTTGTATTTTTGGTAGAGACGGGGTTTCACCATATTGGCCAGGCTGGTCTCCAACTCCT	3986
Query	2435	GACCTCAGTAAATCCGCCCCGCTCGGCCCTCCCAAAATGCTGGGATTACAGGTATGAGCCA	2494
Sbjct	3987	AATCTCAGGTGATCTACCCACCTTGGGCTCCCAAAATGCTGGGATTACAGGCGTGAACCA	4046
Query	2495	CTGGGCCCTTCCCTGTCCTG-IGATTTTAAATAATATACCAGCAGAAGGACGTCCAGA	2553
Sbjct	4047	CTGCTCCCTTCCCTGTCCTTCTGATTTTAAATAACTATACCAGCAGGAGGACGTCCAGA	4106
Query	2554	CACAGCATGGGCTACCTGGCCATGCCAGGCCAGTTGGACATTGAGTTGTTTGCTTGGCA	2613
Sbjct	4107	CACAGCATAGGCTACCTGGCCATGCCAACCGTGGGACATTGAGTTGTTTGCTTGGCA	4166
Query	2614	CTGTCTCTCATGCATTGGGTCCACTCAGTAGAGCTTGTGTTGAATTC	2660
Sbjct	4167	CTGTCTCTCATGCGTGGGTCCACTCAGTAGAGCTTGTGTTGAATTC	4213

Database: Nucleotide sequences derived from the Patent division of GenBank

Posted date: Mar 1, 2009 2:34 AM

Number of letters in database: 537,266,521

Number of sequences in database: 8,753,385

Lambda	K	H
1.33	0.621	1.12

Gapped		
Lambda	K	H
1.28	0.460	0.850

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 0, Extension: 0

Number of Sequences: 8753385

Number of Hits to DB: 1394086

Number of extensions: 628

Number of successful extensions: 628

Number of sequences better than 10: 419

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 603

Number of HSP's successfully gapped: 603

Length of query: 2660

Length of database: 4832233817

Length adjustment: 32

Effective length of query: 2628

Effective length of database: 4552125497

Effective search space: 11962985806116

Effective search space used: 11962985806116

$$A: 0$$

X1: 12 (23.1 bits)

X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 12 (23.3 bits)
S2: 22 (41.7 bits)